WHAT IS CLAIMED IS:

1. An isolated plant promoter comprising at least one synthetic multimeric promoter element region that is capable of driving transcription in a plant cell, wherein said promoter comprises a polynucleotide selected from the group consisting of:

(a) a nucleotide sequence of not greater than 2000 nucleotides comprising promoter elements GT-2 comprising SEQ ID NO.:24, ABRE1 comprising SEQ ID NO.:2, ABRE1 comprising SEQ ID NO.:2, GT-2 comprising SEQ ID NO.:24, As-1 comprising SEQ ID NO.:7, GT-2 comprising SEQ ID NO.:24, GT-2 comprising SEQ ID NO.:24, DRE1 comprising SEQ ID NO.:59, GT-2 comprising SEQ ID NO.:24, DRE1 comprising SEQ ID NO.:59, DRE1 comprising SEQ ID NO.:59, As-1 comprising SEQ ID NO.:7, DRE1 comprising SEQ ID NO.:59, DRE1 comprising SEQ ID NO.:59, and ABRE1 comprising SEQ ID NO.:2, sequentially;

(b) a nucleotide sequence comprising SEQ ID NO.:65;

(c) a nucleotide sequence of not less than 50 nucleotides that hybridizes under stringent conditions to a nucleotide sequence of (a) or (b), wherein said stringent conditions are hybridization in 50% formamide, 1M NaCl, 1% SDS at 37°C, and a wash in 0.1xSSC at 60-65°C; and

(d) a polynucleotide which has at least about 90% sequence identity as determined by the GAP algorithm under default parameters across the full length of a sequence of (a) or to the promoter elements of (b).

2. A chimeric gene comprising the promoter of claim 1 operably linked to a coding sequence.

3. An expression cassette comprising the chimeric gene of claim 2.

4. A transformation vector comprising the expression cassette of claim 3.

5. A plant stably transformed with the transformation vector of claim 4.

6. A plant, or its parts, having stably incorporated into its genome a DNA construct comprising a plant promoter of claim 1 operably linked to a coding sequence.

7. A plant, or its parts, having stably incorporated into its genome a DNA construct comprising a plant promoter operably linked to a coding sequence, said plant promoter comprising at least one synthetic multimeric promoter element region that is capable of driving transcription in a plant cell, wherein said promoter comprises a polynucleotide selected from the group consisting of:

(a) a nucleotide sequence of not greater than 2000 nucleotides comprising promoter elements GT-2 comprising SEQ ID NO.:24, ABRE1 comprising SEQ ID NO.:2, ABRE1 comprising SEQ ID NO.:2, GT-2 comprising SEQ ID NO.:24, As-1 comprising SEQ ID NO.:7, GT-2 comprising SEQ ID NO.:24, GT-2 comprising SEQ ID NO.:24, DRE1 comprising SEQ ID NO.:59, GT-2 comprising SEQ ID NO.:24, DRE1 comprising SEQ ID NO.:59, DRE1 comprising SEQ ID NO.:59, As-1 comprising SEQ ID NO.:7, DRE1 comprising SEQ ID NO.:59, DRE1 comprising SEQ ID NO.:59, and ABRE1 comprising SEQ ID NO.:2, sequentially;

(b) a nucleotide sequence comprising SEQ ID NO.:65;

(c) a nucleotide sequence of not less than 50 nucleotides that hybridizes under stringent conditions to a nucleotide sequence of (a) or (b), wherein said stringent conditions are hybridization in 50% formamide, 1M NaCl, 1% SDS at 37°C, and a wash in 0.1XSSC at 60-65°C; and

(d) a polynucleotide which has at least about 90% sequence identity as determined by the GAP algorithm under default parameters across the full length of a sequence of (a) or to the promoter elements of (b).

8. The plant of claim 7, wherein said plant is a dicot.

9. The plant of claim 7, wherein said plant is a monocot.

10. The plant of claim 9, wherein said monocot is maize.

11. A plant cell having stably incorporated into its genome a DNA construct comprising a plant promoter operably linked to a coding sequence, said plant promoter comprising at least one synthetic multimeric promoter element region that is capable of driving transcription in a plant cell, wherein said promoter comprises a polynucleotide selected from the group consisting of:

(a) a nucleotide sequence of not greater than 2000 nucleotides comprising promoter elements GT-2 comprising SEQ ID NO.:24, ABRE1 comprising SEQ ID NO.:2, ABRE1 comprising SEQ ID NO.:2, GT-2 comprising SEQ ID NO.:24, As-1 comprising SEQ ID NO.:7, GT-2 comprising SEQ ID NO.:24, GT-2 comprising SEQ ID NO.:24, DRE1 comprising SEQ ID NO.:59, GT-2 comprising SEQ ID NO.:24, DRE1 comprising SEQ ID NO.:59, DRE1 comprising SEQ ID NO.:59, As-1 comprising SEQ ID NO.:7, DRE1 comprising SEQ ID NO.:59, DRE1 comprising SEQ ID NO.:59, and ABRE1 comprising SEQ ID NO.:2, sequentially;

(b) a nucleotide sequence comprising SEQ ID NO.:65;

(c) a nucleotide sequence of not less than 50 nucleotides that hybridizes under stringent conditions to the nucleotide sequence of (a) or (b), wherein said stringent conditions are hybridization in 50% formamide, 1M NaCl, 1% SDS at 37°C, and a wash in 0.1XSSC at 60-65°C; and,

(d) a polynucleotide which has at least about 90% sequence identity as determined by the GAP algorithm under default parameters across the full length of a sequence of (a) or to the promoter elements of (b).

12. The plant cell of claim 11, wherein said plant cell is from a dicotyledonous plant.

13. The plant cell of claim 11, wherein said plant cell is from a monocotyledonous plant.

14. The plant cell of claim 13, wherein said monocotyledonous plant is a maize plant.

15. A method for constitutively expressing a heterologous nucleotide sequence in a plant, said method comprising:

(a) transforming a plant cell with a transformation vector comprising an expression cassette, said expression cassette comprising a plant promoter of claim 2 operably linked to a coding sequence ; and

(b) regenerating a stably transformed plant from said transformed cell, said plant having stably incorporated into its genome said expression cassette.